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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO
10/538,001	03/17/2006	Roberto A. Macina	DEX-0548	8198
32800 7590 12/31/2007 LICATA & TYRRELL P.C. 66 E. MAIN STREET			EXAMINER	
			MARTINELL, JAMES	
MARLTON, NJ 08053			ART UNIT	PAPER NUMBER
			1634	
			NOTIFICATION DATE	DELIVERY MODE
			12/31/2007	ELECTRONIC

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Notice of the Office communication was sent electronically on above-indicated "Notification Date" to the following e-mail address(es):

poreilly@licataandtyrrell.com

·	Application No.	Applicant(s)			
	10/538,001	MACINA ET AL.			
Office Action Summary	Examiner	Art Unit			
	James Martinell	1634			
The MAILING DATE of this communication appears on the cover sheet with the correspondence address Period for Reply					
A SHORTENED STATUTORY PERIOD FOR REPLY WHICHEVER IS LONGER, FROM THE MAILING DA - Extensions of time may be available under the provisions of 37 CFR 1.13 after SIX (6) MONTHS from the mailing date of this communication. - If NO period for reply is specified above, the maximum statutory period w - Failure to reply within the set or extended period for reply will, by statute, Any reply received by the Office later than three months after the mailing earned patent term adjustment. See 37 CFR 1.704(b).	ATE OF THIS COMMUN 36(a). In no event, however, may a rill apply and will expire SIX (6) MO cause the application to become	IICATION. a reply be timely filed DNTHS from the mailing date of this communication. ABANDONED (35 U.S.C. § 133).			
Status					
3) Since this application is in condition for allowar closed in accordance with the practice under E	action is non-final. nce except for formal ma				
Disposition of Claims					
4) Claim(s) 1-18 is/are pending in the application. 4a) Of the above claim(s) 11-14 is/are withdraw 5) Claim(s) is/are allowed. 6) Claim(s) 1-10 and 15-18 is/are rejected. 7) Claim(s) is/are objected to. 8) Claim(s) are subject to restriction and/or Application Papers 9) The specification is objected to by the Examine 10) The drawing(s) filed on is/are: a) access applicant may not request that any objection to the Replacement drawing sheet(s) including the correct 11) The oath or declaration is objected to by the Examine	rn from consideration. r election requirement. r. epted or b) □ objected to drawing(s) be held in abey ion is required if the drawir	ance. See 37 CFR 1.85(a). ng(s) is objected to. See 37 CFR 1.121(d).			
Priority under 35 U.S.C. § 119					
12) Acknowledgment is made of a claim for foreign a) All b) Some * c) None of: 1. Certified copies of the priority documents 2. Certified copies of the priority documents 3. Copies of the certified copies of the priority application from the International Bureau * See the attached detailed Office action for a list	s have been received. s have been received in rity documents have bee u (PCT Rule 17.2(a)).	Application No en received in this National Stage			
Attachment(s) 1) ☑ Notice of References Cited (PTO-892) 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948) 3) ☑ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date 6/3/05.	Paper N	v Summary (PTO-413) o(s)/Mail Date f Informal Patent Application 			

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Applicant's election with traverse of the requirement for restriction in the reply filed on November 5, 2007 is acknowledged. The traversal is on the ground(s) that "a search of the art relating to an elected nucleic acid sequence should reveal art relating to the protein encoded thereby and antibodies thereto". This is not found persuasive because the searches of the three Groups of inventions are not coextensive. It is noted that applicants did not argue against the selection of a single sequence for examination on the merits.

The requirement is still deemed proper and is therefore made FINAL.

Claims 11-14, 15 (insofar as it is drawn to polypeptide assays) and 16-18 (insofar as they are drawn to kits containing polypeptides (claim 16), methods of treatment using polypeptides (claim 17), and polypeptide vaccines (claim 18)) are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected invention, there being no allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement in the reply filed on November 5, 2007.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1-10 and 15-18 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. The claims are vague, indefinite, and incomplete.

(a) Claims 1 and 15-18 are vague and indefinite because they claim more than was elected. Claim 1 is drawn to more than one selected nucleic acid sequence. Claim 15 (parts (a)(v) and (vi) and part (b) comparing polypeptide amounts) is drawn to a non-elected invention. Claim 16 (part (e)) is drawn to kits containing polypeptides. Claim 17 (part (e)) is drawn to methods of using polypeptides. Part of claim 18 is drawn to polypeptide vaccines.

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- (b) The recitation of "selectively hybridizes to" (claims 1, 15, and 16) is vague, indefinite, and incomplete because nucleic acid molecular hybridization is a process in which selective hybridization is dependent upon competing target in the hybridization mixture (e.g., see Kennell (Progr. Nucl. Acid Res. Mol. Biol. 11: 259 (1971)) cited here as of interest). Since the claims give no information about the presence or absence of competing targets, the claims are vague, indefinite, and incomplete. The metes and bounds of the claims are not clear.
- incomplete because nucleic acid molecular hybridization is a process in which selective hybridization is dependent upon competing target in the hybridization mixture (e.g., see Kennell (Progr. Nucl. Acid Res. Mol. Biol. 11: 259 (1971)) cited here as of interest). Since the claim gives no information about the presence or absence of competing targets, the claim is vague, indefinite, and incomplete. The metes and bounds of the claim are not clear.
- (d) Claims 16, 17, and 18 are incomplete because they depend from cancelled claim 12.

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless -

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 1-10 and 15-18 are rejected under 35 U.S.C. 102(b) as being clearly anticipated by Rosen et al (WO 00/55350 (September 21, 2000)). SEQ ID NO: 143 of Rosen et al encodes a polypeptide that is 95.3% identical to SEQ ID NO: 174 of the instant claims (see the alignment below). Rosen et al teaches uses of the polynucleotides as cancer therapeutics and cancer markers, including breast cancer

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markers (*e.g.*, see page 375, line 6 through page 381, line 11 (use against cancers); page 346, line 19 through page 356, line 7 (uses of polynucleotides); page 330, line 6 through page 336, line 27 (therapeutic uses)); and gene therapy (page 360, line 12 through page 372, line 4)). Rosen et al also teaches the collection of nucleic acids into kits for convenience (*e.g.*, see page349, line 15 through page 350, line 13).

Alignment of Rosen et al (WO 00/55350 SEQ ID NO: 143) with SEQ ID NO:,70

```
RESULT 5
AAC77749
    AAC77749 standard; cDNA; 1235 BP.
XX
AC
     AAC77749;
XX
DT
     08-FEB-2001 (first entry)
XX
DΕ
     Human cancer associated gene sequence SEQ ID NO:143.
XX
KW
     Human; cancer associated gene; cancer antigen; detection; cancer;
KW
     diagnosis; cytostatic; proliferative; vulnerary; immunomodulator;
     antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
KW
KW
     antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
     dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
KW
     vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
     immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW
     allergic reaction; graft versus host disease; organ rejection;
     haemostatic; thrombolytic; cardiovascular disorder; infection;
KW
KW
     neurological disease; drug screening; ss.
XX
OS
     Homo sapiens.
XX
     WO200055350-A1.
PN
XX
     21-SEP-2000.
PD
XX
     08-MAR-2000; 2000WO-US005882.
PF
XX
     12-MAR-1999;
                    99US-0124270P.
PR
XX
PA
     (HUMA-) HUMAN GENOME SCI INC.
XX
ΡI
     Rosen CA, Ruben SM;
XX
     WPI; 2000-587533/55.
DR
     P-PSDB; AAB43540.
DR
XX
     Novel isolated nucleic acids comprising sequences encoding peptides
PT
     useful for treating or diagnosing e.g. cancer.
PT
XX
     Claim 1; Page 722-723; 2352pp; English.
XX
CC
     AAC77607 to AAC78448 encode the human cancer associated proteins given in
     AAB43398 to AAB44239. The proteins can have activities based on the
CC
CC
     tissues and cells the genes are expressed in. Example of activities
     include: cytostatic; proliferative; vulnerary; immunomodulator;
CC
     antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
CC
     antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
CC
     dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
CC
     nootropic; vasotropic; antipsoriatic and antiangiogenic. The
CC
     polynucleotides and polypeptides can be used for preventing, treating or
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ameliorating medical conditions and diagnosing pathological conditions.
CC
    Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating
CC
    or inhibiting the proliferation, differentiation or mobilisation of
CC
    immune cells, to treat disorders of haematopoietic cells, autoimmune
CC
CC
    disorders, allergic reactions, graft versus host disease and organ
CC
    rejection, modulate haemostatic or thrombolytic activity, modulate
    inflammation, cancers, cardiovascular disorders, neurological disease and
CC
    bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to
CC
CC
    AAC78457 and AAB44240 represent sequences used in the exemplification of
CC
CC
    the present invention
XX
    Sequence 1235 BP; 257 A; 389 C; 394 G; 194 T; 0 U; 1 Other;
SO
Alignment Scores:
Pred. No.:
                    6.53e-111
                                 Length:
                                              1235
Score:
                    1158.00
                                 Matches:
                                              221
Percent Similarity:
                    92.5%
                                 Conservative:
                                              0
Best Local Similarity:
                    92.5%
                                 Mismatches:
Query Match:
                    95.3%
                                 Indels:
                                              18
US-10-538-001-174 (1-224) x AAC77749 (1-1235)
          2 ValProGlyArgTrpArgGlnHisLeuGlnProArgArgArgCysArgSer----- 18
Qy
            GTCCCAGGAAGGTGGCGTCAGCATCTGCAGCCGCGTCGACGTTGTCGGAG-CCTCCGCGG 128
Qу
         19 -----LeuProThrLeuProMetGlu 25
                                              11111111111111111111111
        129 AGGACCCAGGAGAGCCGGACTAGGACCAGGGCCCTGGGCCTCCCCACACTCCCCATGGAG 188
Db
         26 LysLeuAlaAlaSerThrGluProGlnGlyProArgProValLeuGlyArgGluSerVal 45
Qy
            189 AAGCTGGCGGCCTCTACAGAGCCCCAAGGGCCTCGGCCGGTCCTGGGCCGTGAGAGTGTC 248
Db
         46 GlnValProAspAspGlnAspPheArgSerPheArgSerGluCysGluAlaGluValGly 65
Qy
            249 CAGGTGCCCGATGACCAAGACTTTCGCAGCTTCCGGTCAGAGTGTGAGGCTGAGGTGGGC 308
Db
         66 TrpAsnLeuThrTyrSerArgAlaGlyValSerValTrpValGlnAlaValGluMetAsp 85
Qу
            309 TGGAACCTGACCTATAGCAGGGCTGGGGTGTCTGTCTGGGTGCAGGCTGTGGAGATGGAT 368
Db
         86 ArgThrLeuHisLysIleLysCysArgMetGluCysCysAspValProAlaGluThrLeu 105
Qy
            369 CGGACGCTGCACAAGATCAAGTGCCGGATGGAGTGCTGTGATGTGCCAGCCGAGACACTC 428
Db
            TyrAspValLeuHisAspIleGluTyrArgLysLysTrpAspSerAsnValIleGluThr 125
Qу
            429 TACGACGTCCTACACGACATTGAGTACCGCAAGAAATGGGACAGCAACGTCATTGAGACT 488
        126 PheAspIleAlaArgLeuThrValAsnAlaAspValGlyTyrTyrSerTrpArgCysPro 145
Qv
            TTTGACATCGCCCGCTTGACAGTCAACGCTGACGTGGGCTATTACTCCTGGAGGTGTCCC 548
Db
        146 \ {\tt LysProLeuLysAsnArgAspValIleThrLeuArgSerTrpLeuProMetGlyAlaAsp} \ 165
Qy
            549 AAGCCCTGAAGAACCGTGATGTCATCACCCTCCGCTCCTGGCTCCCCATGGGCGCTGAT 608
Db
        166 TyrIleIleMetAsnTyrSerValLysHisProLysTyrProProArgLysAspLeuVal 185
Qy
            609 TACATCATTATGAACTACTCAGTCAAACATCCCAAATACCCACCTCGGAAAGACTTGGTC 668
Db
        186 ArgAlaValSerIleGlnThrGlyTyrLeuIleGlnSerThrGlyProLysSerCysVal 205
Qy
            669 CGAGCTGTGTCCATCCAGACGGGCTACCTCATCCAGAGCACAGGGCCCAAGAGCTGCGTC 728
Db
```

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Claims 1-3, 6, 8, and 9 are rejected under 35 U.S.C. 102(b) as being clearly anticipated by GenBank® Accession No. BE791925 (September 20, 2000). GenBank® Accession No. BE791925 encodes a polypeptide that is 95.3% identical to SEQ ID NO: 174 of the instant claims (see the alignment below). Thus, the polynucleotide of GenBank® Accession No. BE791925 is embraced by the claims.

Alignment of GenBank® Accession No. BE791925 with SEQ ID NO: 70

```
RESULT 1
BE791925
                                                                EST 20-SEP-2000
            BE791925
                                     826 bp
LOCUS
                                               mRNA
                                                       linear
           601585824F1 NIH MGC 7 Homo sapiens cDNA clone IMAGE:3940444 5',
DEFINITION
            mRNA sequence.
            BE791925
ACCESSION
            BE791925.1 GI:10213123
VERSION
KEYWORDS
SOURCE
            Homo sapiens (human)
  ORGANISM
           Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE
            1 (bases 1 to 826)
            NIH-MGC http://mgc.nci.nih.gov/.
  AUTHORS
            National Institutes of Health, Mammalian Gene Collection (MGC)
  TITLE
  JOURNAL
            Unpublished (1999)
COMMENT
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM790 row: o column: 05
            High quality sequence start: 5
            High quality sequence stop: 787.
FEATURES
                     Location/Qualifiers
                     1. .826
     source
                     /organism="Homo sapiens"
                     /mol type="mRNA"
                     /db xref="taxon:9606"
                     /clone="IMAGE:3940444"
                     /tissue type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab host="DH10B (phage-resistant)"
                     /clone lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
```

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```
(Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN
Alignment Scores:
                                       826
Pred. No.:
                 2.57e-115
                            Length:
                            Matches:
                                       221
Score:
                 1189.00
                            Conservative:
Percent Similarity:
                 99.5%
                            Mismatches:
                 99.5%
                                       1
Best Local Similarity:
                 97.9%
Query Match:
                            Indels:
                                       1
                            Gaps:
US-10-538-001-174 (1-224) x BE791925 (1-826)
        3 ProGlyArgTrpArgGlnHisLeuGlnProArgArgArgCysArgSerLeuProThrLeu 22
Qy
          5 CCAGGAAGGTGGCGTCAGCATCTGCAGCCGCGTCGACGTTGTCGGAGCCTCCCCACACTC 64
Db
        23 ProMetGluLysLeuAlaAlaSerThrGluProGlnGlyProArgProValLeuGlyArg 42
Οv
          CCCATGGAGAAGCTGGCGGCCTCTACAGAGCCCCAAGGGCCTCGGCCGGTCCTGGGCCGT 124
Db
        43 GluSerValGlnValProAspAspGlnAspPheArgSerPheArgSerGluCysGluAla 62
Qy
          125 GAGAGTGTCCAGGTGCCCGATGACCAAGACTTTCGCAGCTTCCGGTCAGAGTGTGAGGCT 184
        63 GluValGlyTrpAsnLeuThrTyrSerArgAlaGlyValSerValTrpValGlnAlaVal 82
Qy
          Db
        83 GluMetAspArgThrLeuHisLysIleLysCysArgMetGluCysCysAspValProAla 102
Qy
          245 GAGATGGATCGGACGCTGCACAAGATCAAGTGCCGGATGGAGTGCTGTGATGTGCCAGCC 304
Db
       103 GluThrLeuTyrAspValLeuHisAspIleGluTyrArgLysLysTrpAspSerAsnVal 122
Qу
          305 GAGACACTCTACGACGTCCTACACGACATTGAGTACCGCAAGAAATGGGACAGCAACGTC 364
Db
       123 IleGluThrPheAspIleAlaArqLeuThrValAsnAlaAspValGlyTyrTyrSerTrp 142
Qу
          365 ATTGAGACTTTTGACATCGCCGCTTGACAGTCAACGCTGACGTGGGCTATTACTCCTGG 424
Db
       143 ArqCysProLysProLeuLysAsnArqAspValIleThrLeuArgSerTrpLeuProMet 162
Qy
          425 AGGTGTCCCAAGCCCCTGAAGAACCGTGATGTCATCACCCTCCGCTCCTGGCTCCCCATG 484
Db
       163 GlyAlaAspTyrIleIleMetAsnTyrSerValLysHisProLysTyrProProArgLys 182
Òν
          485 GGCGCTGATTACATCATTATGAACTACTCAGTCAAACATCCCAAATACCCACCTCGGAAA 544
Db
       183 AspLeuValArgAlaValSerIleGlnThrGlyTyrLeuIleGlnSerThrGlyProLys 202
Qy
          545 GACTTGGTCCGAGCTGTGTCCATCCAGACGGGCTACCTCATCCAGAGCACAGGGCCCAAG 604
       203 SerCysValIleThrTyrLeuGlyProGlyGlyProGlnArgLeuLeuThrGlnValGly 222
Οv
          605 AGCTGCGTCATCACCTACCT-GGCCCAGGTGGACCCCAAAGGCTCCTTACCCAAGTGGGT 663
Db
       223 GlyGlu 224
Qу
          HHHH
       664 GGTGAA 669
Db
```

Any inquiry concerning this communication or earlier communications from the examiner should be directed to James Martinell whose telephone number is (571) 272-0719.

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The examiner works a flexible schedule and can be reached by phone and voice mail.

Alternatively, a request for a return telephone call may be e-mailed to <u>james.martinell@uspto.gov</u>. Since e-mail communications may not be secure, it is suggested that information in such requests be limited to

name, phone number, and the best time to return the call.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ram

Shukla, can be reached on (571) 272-0735.

OFFICIAL FAX NUMBER

The fax phone number for the organization where this application or proceeding is assigned is

(571) 273-8300. Any Official Communication to the USPTO should be faxed to this number.

Any inquiry of a general nature or relating to the status of this application or proceeding should

be directed to (571) 272-0547.

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James Martinell, Ph.D Primary Examiner

12/17/07

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